

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: December 14, 2005, 04:20:34 ; Search time 4339.41 Seconds  
(without alignments)  
5024.367 Million cell updates/sec

Title: US-10-674-124A-1  
Perfect score: 466  
Sequence: 1 agatgatgatgatcatgtg.....actgaacgcgcgaatttcag 466

Scoring table:   
Gapop 60.0 , Gapext 60.0

Searched: 41078325 seqs, 23393541228 residues

Word size: 0  
Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Listing first 50 summaries

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6: gb\_est5:\*  
7: gb\_est6:\*  
8: gb\_est7:\*  
9: gb\_gss1:\*  
10: gb\_gss2:\*  
11: gb\_gss3:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	268	57.5	406	5	EX488224 DKFZp686P
2	36	7.7	217	11	FR0012565
3	36	7.7	596	11	FR0012561
4	29	6.2	915	11	CNS04H62
5	29	6.2	1055	11	CNS03K08
6	28	6.0	261	2	BF910800
7	28	6.0	301	7	CV342994
8	28	6.0	618	10	CE424277
9	28	6.0	908	11	CR076016
10	27	5.8	491	11	CNS044H0
11	27	5.8	595	9	AQ602695
12	27	5.8	601	11	FR0012542
13	27	5.8	796	9	BZ149254
14	27	5.8	1101	11	CNS05PWW
15	26	5.6	547	11	CR254696
16	26	5.6	549	10	CE494613
17	26	5.6	578	9	BH258010
18	26	5.6	598	10	BX194414
19	26	5.6	678	10	CE586092
20	26	5.6	844	11	CNS04QD0
21	26	5.6	968	11	CNS052LN
22	26	5.6	1027	10	CNS02PUN

23	25	5.4	237	9	BH055972
24	25	5.4	416	6	CB767615
25	25	5.4	492	9	AZ442057
26	25	5.4	498	6	CF608447
27	25	5.4	498	6	CF609035
28	25	5.4	498	6	CF609040
29	25	5.4	498	10	CE309451
30	25	5.4	547	9	AZ823003
31	25	5.4	576	9	AZ840510
32	25	5.4	641	9	BH091021
33	25	5.4	753	10	AG459390
34	25	5.4	902	11	CR105359
35	25	5.4	1030	11	CNS04T8S
36	25	5.4	1057	11	CNS05PZY
37	25	5.4	2998	4	AK043931
38	25	5.2	209	3	BM005463
39	24	5.2	231	3	BM026778
40	24	5.2	338	11	CR918692
41	24	5.2	398	10	CE767847
42	24	5.2	423	1	AV726011
43	24	5.2	433	9	AQ090767
44	24	5.2	434	9	BZ263771
45	24	5.2	498	10	CE725139
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ALIGNMENTS

RESULT 1

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

406 bp mRNA linear EST 04-SEP-2003  
DKFZp686P23268\_r1 686 (synonym: hlcc3) Homo sapiens cDNA clone  
DKFZp686P23268\_5', mRNA sequence.  
BX488224  
BX488224  
EST.  
Homo sapiens (human)  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.  
1 (bases 1 to 406)  
Bahr, A., Lauber, J., Mewes, H.W., Weil, B., Amid, C., Osanger, A.,  
Fobo, G., Han, M. and Wiemann, S.  
EST (Bahr, A., Lauber, J., Mewes, H.W., Weil, B., et al.)  
Unpublished (2003)  
Contact: MIPS  
MIPS  
Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany  
This is the 5' sequence of the clone insert  
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer  
Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;  
sequenced by Qiagen (Hilden/Germany) within the cDNA sequencing  
consortium of the German Genome Project.  
No si sequence available.  
This clone (DKFZp686P23268) is available at the RZPD in Berlin.  
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059  
Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.

FEATURES

source

1..406  
/organism="Homo sapiens"  
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/lab\_lib="686 (synonym: hlcc3)"  
/note="Vector: pTriplex2; Site\_1: SfiIA; Site\_2: SfiIB;



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OM nucleic - nucleic search, using sw model

Run on: December 14, 2005, 03:13:04 ; Search time 515.162 Seconds  
(without alignments)  
6028.680 Million cell updates/sec

Title: US-10-674-124A-1  
Perfect score: 466  
Sequence: 1 agatgatgatgatgcattg.....actgaaacgtggaatttcag 466

Scoring table: OLIGO NUC  
Gapop 60.0, Gapext 60.0

Searched: 4996997 seqs, 332346308 residues

Word size: 0

Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Listing first 50 summaries

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13: Geneseqn2004bs:.\*  
14: Geneseqn2005s:.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	31	6.7	76644	12	ADQ97602 Mouse can
2	26	5.6	151858	13	ABD33489 Murine ca
3	25	5.4	8222	8	ACF62815 Colon can
4	25	5.4	8222	8	ACF62793 Colon can
5	25	5.4	11222	10	ADB54189 Pretreat
6	25	5.4	11222	10	ADB54317 Pretreat
7	24	5.2	393	4	AAI87991 Human pol
8	24	5.2	4372	10	ADD48700 Rat gene
9	24	5.2	24281	13	ABD33480 Murine ca
10	24	5.2	24281	14	AD213479 Murine ca
11	24	5.2	95835	11	ACN45042 Human gen
12	24	5.2	110000	13	ABD32804 Continuation (5 of
13	23	4.9	551	6	ABN60833 Human can
14	23	4.9	6731	6	ABK39962 Human che
15	23	4.9	85920	14	AD213418 Human can
16	22	4.7	355	2	AAX33665 DNA cand
17	22	4.7	397	6	ABN79099 Human ORF
18	22	4.7	519	12	ACH76810 Human gen
19	22	4.7	26502	12	ADL18577 Human wil

C	20	22	4.7	39071	12	ADM97420	Prostate
C	21	22	4.7	42952	13	ABD33609	Abd33609 Murine ca
C	22	22	4.7	46275	6	ABT10145	Abt10145 Human bre
C	23	22	4.7	46275	10	ADL13621	Adl13621 Osteoarth
C	24	22	4.7	88232	11	ACN44980	Acn44980 Mouse gen
C	25	22	4.7	96596	10	ADE95968	Ades95968 Human NFA
C	26	22	4.7	96597	9	ADA02720	Ada02720 Human NFA
C	27	22	4.7	96597	10	ADB72458	Adb72458 Human NFA
C	28	22	4.7	96597	8	ACF62734	Acf62734 Cancer ba
C	29	22	4.7	96960	8	ADB20849	Adb20849 MRP1 base
C	30	22	4.7	96960	10	ADB87938	Adb87938 Human UGT
C	31	22	4.7	96960	10	ADB96921	Adb96921 Human UGT
C	32	22	4.7	96960	10	ADB92112	Adb92112 Human MDR
C	33	22	4.7	100534	13	ABD32647	Abd32647 Mouse can
C	34	22	4.7	107432	12	ADQ97161	Adq97161 Mouse can
C	35	22	4.7	114771	12	ADQ17641	Adq17641 Human sof
C	36	22	4.7	123785	10	ABX77171	Abx77171 DNA seque
C	37	22	4.7	159001	12	ADL17884	Adl17884 Human pho
C	38	22	4.7	165156	13	ADS36459	Ads36459 Human aut
C	39	22	4.7	173564	13	ABD32953	Abd32953 Human can
C	40	22	4.7	183610	8	ACF62736	Acf62736 Cancer ba
C	41	22	4.7	183610	8	ADB20851	Adb20851 MRP1 base
C	42	22	4.7	183610	10	ADB87940	Adb87940 Human UGT
C	43	22	4.7	183610	10	ADB96923	Adb96923 Human MDR
C	44	22	4.7	183610	10	ADB92114	Adb92114 Human MDR
C	45	22	4.7	186591	8	ACF62750	Acf62750 Cancer ba
C	46	22	4.7	186591	8	ADB20869	Adb20869 MRP1 base
C	47	22	4.7	186591	10	ADB87958	Adb87958 Human UGT
C	48	22	4.7	186591	10	ADB96941	Adb96941 Human MDR
C	49	22	4.7	186591	10	ADB92132	Adb92132 Human MDR
C	50	22	4.7	208648	8	ACF62735	Acf62735 Cancer ba

ALIGNMENTS

RESULT 1  
ADQ97602  
ID ADQ97602 standard; DNA; 76644 BP.  
XX  
AC ADQ97602;  
XX  
DT 07-OCT-2004 (first entry)  
XX  
DE Mouse cancer associated sequence MD10-013, SEQ ID 579.  
XX  
KW Cytostatic; Gene Therapy; cancer; leukemia; lymphoma; Mouse; ds.  
XX  
OS Mus musculus.  
XX  
PN WO2004060304-A2.  
XX  
PD 22-JUL-2004.  
XX  
PF 22-DEC-2003; 2003WO-US041389.  
XX  
PR 27-DEC-2002; 2002US-00330773.  
XX  
PA (SAGR-) SAGRES DISCOVERY INC.  
PI Morris DW, Malandro MS;  
XX  
WPI; 2004-543781/52.  
XX  
PT New isolated cancer associated nucleic acids comprising at least 10 contiguous nucleotides, useful for diagnosing, preventing and/or treating cancers such as leukemia and lymphoma.  
XX  
PS Claim 1; SEQ ID NO 579; 199pp; English.  
XX  
CC The present invention relates to cancer associated sequences (ADQ97025-ADQ98004). The sequences are useful for the diagnosis, prevention and/or treatment of cancer, such as leukemia and lymphoma. Note: The sequence



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OM nucleic - nucleic search, using sw model

Run on: December 14, 2005, 03:22:04 ; Search time 151.64 Seconds  
(without alignments) 5462.552 Million cell updates

Title: US-10-674-124A-1  
Perfect score: 466  
Sequence: 1 acatgaatgaatagatcattg.....actgaacgtcgaatttcag 466

Scoring table: OLIGO NUC

Searched: 1303057 seqs, 888780828 residues

Word size: 20  
Total number of bits satisfying chosen parameters: 2606114

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Minimum DB seq length: 0
Maximum DB seq length: 20000000000
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Post-processing: Listing first 50 summaries

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pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query		DB	ID	Description
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C	1	27	5, 8	85850	3	US-09-949-016-13424
	2	25	5, 4	601	3	US-09-949-016-175240
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	4	25	5, 4	20662	3	US-09-949-016-16717
C	5	24	5, 2	7868	9	5175383-1
	6	23	4, 9	59719	3	US-09-949-016-15616
C	7	22	4, 7	355	3	US-09-157-177-130
C	8	22	4, 7	355	3	US-09-541-210-130
C	9	22	4, 7	601	3	US-09-949-016-34367
C	10	22	4, 7	601	3	US-09-949-016-34368
C	11	22	4, 7	601	3	US-09-949-016-66532
C	12	22	4, 7	601	3	US-09-949-016-66533
C	13	22	4, 7	601	3	US-09-949-016-71600
C	14	22	4, 7	31197	3	US-09-949-016-12963
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	16	22	4, 7	46885	3	US-09-949-016-13848
	17	22	4, 7	91559	3	US-09-949-016-12581
C	18	22	4, 7	91559	3	US-09-949-016-13701
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## ALIGNMENTS

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RESULT 1
US-09-949-016-13424/c
; Sequence 13424, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH DETECTION OF HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
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; LENGTH: 85850
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; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(85850)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-13424

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RESULT 2
US-09-949-016-175240
; Sequence 175240, Application US/09949016
; Patent No. 6812339

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; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 175240
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; ORGANISM: Human
US-09-949-016-175240

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; Sequence 175241, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
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; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-175241

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Best Local Similarity 100.0%; Pred. No. 0.014;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 93 TGATTGATAGTAGGTAGTAGTAG 117
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RESULT 4
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; Sequence 16717, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
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; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
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; SEQ ID NO 16717
; LENGTH: 20662
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-16717

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Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 93 TGATTGATAGTAGGTAGTAGTAG 117
Db 6351 TGATTGATAGTAGGTAGTAGTAG 6375

RESULT 5
5175383-1/c
; Patent No. 5175383
; APPLICANT: LEDER, PHILIP;MULLER, WILLIAM J.
; TITLE OF INVENTION: ANIMAL MODEL FOR BENIGN PROSTATIC DISEASE
; NUMBER OF SEQUENCES: 9
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/312,641
; FILING DATE: 17-FEB-1989
; SEQ ID NO:1
; LENGTH: 7868
5175383-1

Query Match          5.2%; Score 24; DB 9; Length 7868;
Best Local Similarity 100.0%; Pred. No. 0.039;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 206 GATAGATGGATGGATGGATGGATAG 229
Db 5087 GATAGATGGATGGATGGATGGATAG 5064

RESULT 6
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; Sequence 15616, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 15616
; LENGTH: 59719
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(59719)
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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: December 14, 2005, 06:01:45 ; Search time 361.444 Seconds  
(without alignments)  
631.944 Million cell updates/sec

Title: US-10-674-124A-1  
Perfect score: 466  
Sequence: 1 agatgatgatgatcattg.....actgaacgtcgatttcag 466

Scoring table: OLIGO NUC  
Gapop 60.0 , Gapext 60.0

Searched: 4161359 seqs, 245077644 residues

Word size : 0

Total number of hits satisfying chosen parameters: 8322718

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Listing first 50 summaries

Database : Published Applications NA New:  
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2: /cgn2\_6/ptodata/1/pubpna/US06\_NEW\_PUB.seq:  
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10: /cgn2\_6/ptodata/1/pubpna/US60\_NEW\_PUB.seq:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	22	4.7	165156	6	US-10-995-561-13304
2	21	4.5	201	6	US-10-995-561-20634
3	21	4.5	1548	6	US-10-750-185-34790
4	21	4.5	13943	9	US-11-012-762-39
5	21	4.5	44718	6	US-10-995-561-13217
6	21	4.5	169495	7	US-11-121-086-61
7	21	4.5	169725	7	US-11-121-086-63
8	21	4.5	200628	7	US-11-121-086-62
9	20	4.3	201	6	US-10-995-561-20635
10	20	4.3	201	6	US-10-995-561-23773
11	20	4.3	201	6	US-10-995-561-28163
12	20	4.3	201	6	US-10-995-561-30516
13	20	4.3	201	6	US-10-995-561-47793
14	20	4.3	201	6	US-10-995-561-47795
15	20	4.3	201	6	US-10-995-561-47798
16	20	4.3	201	6	US-10-995-561-47801
17	20	4.3	201	6	US-10-995-561-47804
18	20	4.3	201	6	US-10-995-561-47808
19	20	4.3	201	6	US-10-995-561-47812
20	20	4.3	201	6	US-10-995-561-47816
21	20	4.3	201	6	US-10-995-561-77732
22	20	4.3	1357	6	US-10-750-185-57399
23	20	4.3	1413	6	US-10-750-185-57194

C 24	20	4.3	1632	6	US-10-750-185-58027	Sequence 58027, A
C 25	20	4.3	1935	6	US-10-750-185-51171	Sequence 51171, A
C 26	20	4.3	2103	6	US-10-750-185-29643	Sequence 29643, A
C 27	20	4.3	2129	7	US-11-108-528-33	Sequence 33, Appl
C 28	20	4.3	2231	6	US-10-750-185-34561	Sequence 34561, A
C 29	20	4.3	31973	6	US-10-995-561-13229	Sequence 13229, A
C 30	20	4.3	52192	6	US-10-995-561-13231	Sequence 13231, A
C 31	20	4.3	110847	7	US-11-121-086-11	Sequence 11, Appl
C 32	20	4.3	119160	7	US-11-121-086-12	Sequence 12, Appl
C 33	20	4.3	150468	7	US-11-112-908-56	Sequence 56, Appl
C 34	20	4.3	162537	7	US-11-121-086-59	Sequence 59, Appl
C 35	20	4.3	175673	7	US-11-121-086-55	Sequence 55, Appl
C 36	20	4.3	177175	7	US-11-121-086-79	Sequence 79, Appl
C 37	20	4.3	180654	7	US-11-121-086-58	Sequence 58, Appl
C 38	20	4.3	187786	6	US-10-995-561-13474	Sequence 13474, A
C 39	20	4.3	187986	6	US-10-995-561-13252	Sequence 13252, A
C 40	20	4.3	193789	7	US-11-112-908-55	Sequence 55, Appl
C 41	20	4.3	222094	6	US-10-995-561-13244	Sequence 13244, A
C 42	20	4.3	285300	6	US-10-857-780-6	Sequence 6, Appl
C 43	20	4.3	645179	6	US-10-995-561-13293	Sequence 13293, A
C 44	20	4.3	1125000	6	US-10-995-561-13286	Sequence 13286, A
C 45	19	4.1	201	6	US-10-995-561-23615	Sequence 23615, A
C 46	19	4.1	201	6	US-10-995-561-23805	Sequence 23805, A
C 47	19	4.1	201	6	US-10-995-561-43973	Sequence 43973, A
C 48	19	4.1	201	6	US-10-995-561-43974	Sequence 43974, A
C 49	19	4.1	201	6	US-10-995-561-44636	Sequence 44636, A
C 50	19	4.1	201	6	US-10-995-561-44637	Sequence 44637, A

ALIGNMENTS

RESULT 1  
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; Publication No. US20050272054A1  
; GENERAL INFORMATION:  
; APPLICANT: CARGILL, Michele et al.  
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH  
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF  
; TITLE OF INVENTION: DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001559  
; CURRENT APPLICATION NUMBER: US/10/995,561  
; CURRENT FILING DATE: 2004-11-24  
; NUMBER OF SEQ ID NOS: 85702  
; SOFTWARE: FastSeq for Windows Version 4.0  
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; LENGTH: 165156  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
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DB 124971 GATAGTGGATGGATGGATGAT 124992  
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; Sequence 20634, Application US/10995561  
; Publication No. US20050272054A1  
; GENERAL INFORMATION:  
; APPLICANT: CARGILL, Michele et al.  
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH  
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF  
; TITLE OF INVENTION: DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001559  
; CURRENT APPLICATION NUMBER: US/10/995,561  
; CURRENT FILING DATE: 2004-11-24

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; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 20634
; LENGTH: 201
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-995-561-20634

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Db 76 GTAGATAGATGATGATGGAT 96

RESULT 3
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; Sequence 34790, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM11100-2
; CURRENT APPLICATION NUMBER: US/10/750,185
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 34790
; LENGTH: 1548
; TYPE: DNA
; ORGANISM: Bovine 19866880504043
US-10-750-185-34790

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Best Local Similarity 100.0%; Pred. No. 0.17;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 206 GATAGTGGATGGATGGATGA 226
Db 1198 GATAGTGGATGGATGGATGA 1178

RESULT 4
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; Sequence 39, Application US/11012762
; Publication No. US20050244815A1
; GENERAL INFORMATION:
; APPLICANT: Georgia State University Research Foundation, Inc.
; TITLE OF INVENTION: Compositions and Methods for Viral Resistance Genes
; FILE REFERENCE: GSU1.PCT
; CURRENT APPLICATION NUMBER: US/11/012,762
; CURRENT FILING DATE: 2004-12-15
; PRIOR APPLICATION NUMBER: PCT/US03/19300
; PRIOR FILING DATE: 2003-06-19
; PRIOR APPLICATION NUMBER: US 60/390,046
; PRIOR FILING DATE: 2002-06-19
; NUMBER OF SEQ ID NOS: 133
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 39
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; ORGANISM: Mus musculus
; FEATURE:
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; FEATURE:
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; LOCATION: (12252)..(12350)
US-11-012-762-39

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Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 205 TGATAGTGGATGGATGGATG 225
Db 3155 TGATAGTGGATGGATGGATG 3135

RESULT 5
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; Sequence 13217, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13217
; LENGTH: 44718
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-995-561-13217

Query Match      4.5%; Score 21; DB 6; Length 44718;
Best Local Similarity 100.0%; Pred. No. 0.19;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 328 GTAGATAGATGATGATGGAT 348
Db 26622 GTAGATAGATGATGATGGAT 26642

RESULT 6
US-11-121-086-61
; Sequence 61, Application US/11121086
; Publication No. US20050286459A1
; GENERAL INFORMATION:
; APPLICANT: POULSEN, TIM S.
; APPLICANT: NIELSEN, KIRSTEN V.
; TITLE OF INVENTION: NUCLEIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES
; FILE REFERENCE: 09138.6000-00000
; CURRENT APPLICATION NUMBER: US/11/121,086
; CURRENT FILING DATE: 2005-05-04
; PRIOR APPLICATION NUMBER: 60/567,570
; PRIOR FILING DATE: 2004-05-04
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 61
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GenCore version 5.1.6  
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Gapop 60.0, Gapext 60.0

Searched: 5883141 seqs, 28421725653 residues

Word size : 0  
Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0  
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Post-processing: Listing first 50 summaries

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6: gb\_pat.\*  
7: gb\_ph.\*  
8: gb\_pr.\*  
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15: gb\_pi.\*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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C 2	466	100.0	179567	8 AL669831	AL669831 Human DNA
C 3	244	52.4	701	10 HUMUT7925	L30383 Human STS U
C 4	92	19.7	389	10 AB144915	AB144915 Homo sapi
C 5	92	19.7	85404	8 AC008165	AC008165 Homo sapi
C 6	92	19.7	169754	8 AC103954	AC103954 Homo sapi
C 7	92	19.7	175263	8 AC136777	AC136777 Homo sapi
C 8	65	13.9	70720	14 AC027823	AC027823 Homo sapi
C 9	57	12.2	148535	14 AF166490	AF166490 Homo sapi
C 10	32	6.9	173965	9 AC135673	AC135673 Mus muscu
C 11	32	6.9	204505	14 AC119344	AC119344 Rattus no
C 12	31	6.7	68336	14 AC100653	AC100653 Mus muscu
C 13	31	6.7	110000	14 AC151851_0	AC151851 Takifugu
C 14	31	6.7	112785	9 AL929332	AL929332 Mouse DNA
C 15	31	6.7	125681	9 AC122889	AC122889 Mus muscu
C 16	31	6.7	142195	5 AL844597	AL844597 Zebrafish
C 17	31	6.7	159743	9 AC153971	AC153971 Mus muscu
C 18	31	6.7	164582	9 AC153899	AC153899 Mus muscu

C 19	31	6.7	185068	9 AC157093	AC157093 Mus muscu
C 20	31	6.7	213959	14 AC102642	AC102642 Mus muscu
C 21	31	6.7	228313	14 AC097557	AC097557 Rattus no
C 22	31	6.7	231928	14 AC135680	AC135680 Rattus no
C 23	31	6.7	232002	9 AC153587	AC153587 Mus muscu
C 24	31	6.7	233830	9 AC122223	AC122223 Mus muscu
C 25	31	6.7	241738	14 AC094839	AC094839 Rattus no
C 26	31	6.7	244928	14 AC097177	AC097177 Rattus no
C 27	31	6.7	245125	14 AC133759	AC133759 Rattus no
C 28	31	6.7	246646	14 AC095667	AC095667 Rattus no
C 29	31	6.7	247269	14 AC120819	AC120819 Rattus no
C 30	31	6.7	251286	14 AC125835	AC125835 Rattus no
C 31	31	6.7	272329	14 AC094789	AC094789 Rattus no
C 32	30	6.4	163243	8 HSJ906P16	AL079339 Human DNA
C 33	30	6.4	163243	8 HSJ906P16	AL513304 Human DNA
C 34	30	6.4	213624	14 AC129630	AC129630 Rattus no
C 35	30	6.4	238725	14 AC115260	AC115260 Rattus no
C 36	30	6.4	239049	14 AC111870	AC111870 Rattus no
C 37	29	6.2	74149	14 AC123879_3	Continuation (4 of
C 38	29	6.2	76522	14 AC160993	AC160993 Mus muscu
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C 42	29	6.2	150925	8 AC113607	AC113607 Homo sapi
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C 45	29	6.2	211422	8 AC073493	AC073493 Homo sapi
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C 47	28	6.0	110000	14 AC151851_1	Continuation (2 of
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## ALIGNMENTS

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Homo sapiens chromosome 8 clone RP11-112904, WORKING DRAFT  
SEQUENCE, 45 unordered pieces.

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HTG; HTGS PHASE1; HTGS\_DRAFT; HTGS\_CANCELLED.  
Homo sapiens (human)

Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominiidae; Homo.

1 (bases 1 to 144432)  
Schilhabel,M.B., Baumgart,C., Blechschmidt,K., Dette,M., Jahn,N.,  
Lehmann,R., Menzel,U., Polley,A., Reichwald,K., Schudy,A.,  
Siddiqui,R., Taudien,S., Wen,G., Rosenthal,A. and Platzner,M.  
Chromosome 8 genomic sequence

Unpublished

2 (bases 1 to 144432)

Genome Sequencing Center Jena.

Direct Submission

Submitted (09-JUN-2000) Genome Analysis, Institute of Molecular

Biotechnology, Beutenbergstr. 11, Jena 07745, Germany

On Jun 7, 2001 this sequence version replaced gi:8575834.

----- Genome Center

Center: Institute of Molecular Biotechnology

Center code: IMB

Web site: <http://genome.imb-jena.de/>

Contact: [gscl-submit@genome.imb-jena.de](mailto:gscl-submit@genome.imb-jena.de)

----- Project Information

Center project name: H502

Center clone name: RP11-112904

----- Summary Statistics

Sequencing vector: M13; 100% of reads

Chemistry: Dye-terminator Big Dye; 100% of reads

Assembly program: Phrap; version 0.990329  
 Consensus quality: 112528 bases at least Q40  
 Consensus quality: 121546 bases at least Q30  
 Consensus quality: 129443 bases at least Q20  
 Quality coverage: 3,46 in Q20 bases; sum-of-contigs  
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 \* NOTE: This is a 'working draft' sequence. It currently  
 \* consists of 45 contigs. The true order of the pieces  
 \* is not known and their order in this sequence record is  
 \* arbitrary. Gaps between the contigs are represented as  
 \* runs of N, but the exact sizes of the gaps are unknown.  
 \* This record will be updated with the finished sequence.  
 \* as soon as it is available and the accession number will  
 \* be preserved.

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* 4819: contig of 14579 bp in length
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* 19498: 30809: contig of 11312 bp in length
* 30810: 39009: gap of unknown length
* 30910: 39338: contig of 3029 bp in length
* 33939: 34038: gap of unknown length
* 34039: 36066: contig of 2028 bp in length
* 36067: 36166: gap of unknown length
* 36167: 43662: contig of 10196 bp in length
* 46363: 48462: gap of unknown length
* 46463: 55091: contig of 8629 bp in length
* 55092: 55191: gap of unknown length
* 55192: 60456: contig of 5265 bp in length
* 60457: 60556: gap of unknown length
* 60557: 68575: contig of 6019 bp in length
* 66675: 66675: gap of unknown length
* 66676: 69772: contig of 3097 bp in length
* 69773: 69872: gap of unknown length
* 69873: 76552: contig of 6680 bp in length
* 76553: 76652: gap of unknown length
* 76653: 80187: contig of 3535 bp in length
* 80188: 80287: gap of unknown length
* 80288: 83019: contig of 2732 bp in length
* 83020: 83119: gap of unknown length
* 83120: 86635: contig of 3516 bp in length
* 86636: 86735: gap of unknown length
* 86736: 91292: contig of 4557 bp in length
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* 104083: 104182: gap of unknown length
* 104183: 105396: contig of 1214 bp in length
* 105397: 105496: gap of unknown length
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* 106966: 107066: gap of unknown length
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* 108111: 108210: gap of unknown length
* 108211: 109692: contig of 1482 bp in length
* 109693: 109792: gap of unknown length
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* 114265: 114364: gap of unknown length
* 114365: 115643: contig of 1279 bp in length
* 115644: 115743: gap of unknown length
* 115744: 116958: contig of 1215 bp in length
* 116959: 117058: gap of unknown length
* 117059: 118478: contig of 1420 bp in length
* 118479: 118578: gap of unknown length
* 118579: 119911: contig of 1333 bp in length

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* 119912 120011: gap of unknown length
* 120012 121916: contig of 1905 bp in length
* 121917 122016: gap of unknown length
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* 123283 123382: gap of unknown length
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* 126832 128210: contig of 1379 bp in length
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* 129578 129677: gap of unknown length
* 129678 131529: contig of 1852 bp in length
* 131530 131629: gap of unknown length
* 131630 132683: contig of 1054 bp in length
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* 132784 134301: contig of 1518 bp in length
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* 134402 136280: contig of 1859 bp in length
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* 136361 137553: contig of 1193 bp in length
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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

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Scoring table: POLYGNUG

Gapop 60.0 , Gapext 60.0

Searched: 4161359 seqs, 245077644 residues

Word size: 10

Total number of hits satisfying chosen parameters: 8322718

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 50 summaries

Database : Published Applications NA New:\*

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- 3: /cgn2\_6/ptodata/1/pubpna/US07\_NEW\_PUB\_seq.\*
- 4: /cgn2\_6/ptodata/1/pubpna/US08\_NEW\_PUB\_seq.\*
- 5: /cgn2\_6/ptodata/1/pubpna/PCT\_NEW\_PUB\_seq.\*
- 6: /cgn2\_6/ptodata/1/pubpna/US10\_NEW\_PUB\_seq.\*
- 7: /cgn2\_6/ptodata/1/pubpna/US11\_NEW\_PUB\_seq.\*
- 8: /cgn2\_6/ptodata/1/pubpna/US11\_NEW\_PUB\_seq.\*
- 9: /cgn2\_6/ptodata/1/pubpna/US11\_NEW\_PUB\_seq.\*
- 10: /cgn2\_6/ptodata/1/pubpna/US60\_NEW\_PUB\_seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	30	14.5	169047	7	US-11-121-086-15
2	29	14.0	2443	7	US-10-750-185-40370
3	27	13.0	201	6	US-10-995-561-33632
4	27	13.0	201	6	US-10-995-561-33668
5	27	13.0	201	6	US-10-995-561-76924
6	27	13.0	201	6	US-10-995-561-76927
7	27	13.0	201	6	US-10-995-561-77405
8	27	13.0	201	6	US-10-995-561-31742
9	27	13.0	1338	6	US-10-750-185-58661
10	27	13.0	1879	6	US-10-750-185-38372
11	27	13.0	1968	6	US-10-750-185-24617
12	27	13.0	2090	6	US-10-750-185-51962
13	27	13.0	3098	6	US-10-750-185-46414
14	27	13.0	3238	6	US-10-750-185-38644
15	27	13.0	110711	6	US-10-995-561-13264
16	27	13.0	1477003	7	US-10-857-780-3
17	27	13.0	176503	7	US-11-121-086-53
18	27	13.0	394468	6	US-10-995-561-13473
19	26	12.6	600	6	US-10-750-185-3422
20	26	12.6	888	6	US-10-750-185-35928
21	26	12.6	1085	6	US-10-750-185-28972
22	26	12.6	1089	6	US-10-750-185-40317
23	26	12.6	1488	6	US-10-750-185-60015

c	24	26	12.6	1500	6	US-10-750-185-24893	Sequence 24893, A
c	25	26	12.6	1626	6	US-10-750-185-42949	Sequence 42949, A
c	26	26	12.6	1768	6	US-10-750-185-48978	Sequence 48978, A
c	27	26	12.6	1806	6	US-10-750-185-49853	Sequence 49853, A
c	28	26	12.6	1911	6	US-10-750-185-42482	Sequence 42482, A
c	29	26	12.6	1973	6	US-10-750-185-64418	Sequence 64418, A
c	30	26	12.6	2174	6	US-10-750-185-31781	Sequence 31781, A
c	31	26	12.6	2386	6	US-10-750-185-28178	Sequence 28178, A
c	32	26	12.6	2822	6	US-10-750-185-28046	Sequence 28046, A
c	33	26	12.6	2859	6	US-10-750-185-60847	Sequence 60847, A
c	34	26	12.6	3015	6	US-10-750-185-48995	Sequence 48995, A
c	35	26	12.6	3336	6	US-10-750-185-45825	Sequence 45825, A
c	36	26	12.6	3581	6	US-10-750-185-55045	Sequence 55045, A
c	37	26	12.6	56448	6	US-10-995-561-13359	Sequence 13359, A
c	38	26	12.6	60844	6	US-10-995-561-13359	Sequence 13359, A
c	39	26	12.6	66131	6	US-10-995-561-13501	Sequence 13501, A
*	40	26	12.6	119160	7	US-11-121-086-12	Sequence 12, Appl
c	41	26	12.6	179666	7	US-11-121-086-67	Sequence 67, Appl
c	42	26	12.6	207600	7	US-11-112-908-31	Sequence 31, Appl
c	43	26	12.6	403278	6	US-10-995-561-13421	Sequence 13421, A
c	44	25	12.1	201	6	US-10-995-561-9503	Sequence 9503, Ap
c	45	25	12.1	201	6	US-10-995-561-9519	Sequence 9519, Ap
c	46	25	12.1	201	6	US-10-995-561-51200	Sequence 51200, A
c	47	25	12.1	201	6	US-10-995-561-53066	Sequence 53066, A
c	48	25	12.1	201	6	US-10-995-561-55588	Sequence 55588, A
c	49	25	12.1	201	6	US-10-995-561-75984	Sequence 75984, A
c	50	25	12.1	766	6	US-10-750-185-55672	Sequence 55672, A

ALIGNMENTS

RESULT 1

US-11-121-086-15  
; Sequence 15, Application US/11121086  
; Publication No. US20050266459A1  
; GENERAL INFORMATION:  
; APPLICANT: POULSEN, TIM S.  
; APPLICANT: NIELSEN, KIRSTEN V.  
; TITLE OF INVENTION: NUCLEIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES  
; FILE REFERENCE: 09138.6000-00000  
; CURRENT APPLICATION NUMBER: US/11/121,086  
; CURRENT FILING DATE: 2005-05-04  
; PRIOR APPLICATION NUMBER: 60/567,570  
; PRIOR FILING DATE: 2004-05-04  
; NUMBER OF SEQ ID NOS: 107  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 15  
; LENGTH: 169047  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-11-121-086-15

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Best Local Similarity 100.0%; Pred. No. 4.2e-07;  
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 51 CACACACACACATGTCACGCACACACA 80  
Db 39337 CACACACACACATGTCACGCACACACA 39366

RESULT 2

US-10-750-185-40370  
; Sequence 40370, Application US/10750185  
; Publication No. US20050260603A1  
; GENERAL INFORMATION:  
; APPLICANT: MMI GENOMICS, INC.  
; APPLICANT: DENISE, Sue K.  
; APPLICANT: KERR, Richard  
; APPLICANT: ROSENFELD, David  
; APPLICANT: HOLM, Tom  
; APPLICANT: BATES, Stephen

```
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM11100-2
; CURRENT APPLICATION NUMBER: US/10/750,185
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 40370
; LENGTH: 2443
; TYPE: DNA
; ORGANISM: Bovine 19866880503606
US-10-750-185-40370

Query Match 14.0%; Score 29; DB 6; Length 2443;
Best Local Similarity 100.0%; Pred. No. 1.9e-06;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 36 AGGCACGCGCACACACACACACACACA 64
Db 2396 AGGCACGCGCACACACACACACACACA 2424

RESULT 3
US-10-995-561-33632
; Sequence 33632, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 33632
; LENGTH: 201
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-995-561-33632

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Best Local Similarity 100.0%; Pred. No. 2.7e-05;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 45 CACACACACACACACACATGCACAC 71
Db 113 CACACACACACACACACATGCACAC 139

RESULT 4
US-10-995-561-33668
; Sequence 33668, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 33668
; LENGTH: 201
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-995-561-33668

Query Match 13.0%; Score 27; DB 6; Length 201;
Best Local Similarity 100.0%; Pred. No. 2.7e-05;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 45 CACACACACACACACACATGCACAC 71
Db 104 CACACACACACACACACATGCACAC 130

RESULT 5
US-10-995-561-76924
; Sequence 76924, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 76924
; LENGTH: 201
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-995-561-76924

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Best Local Similarity 100.0%; Pred. No. 2.7e-05;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 45 CACACACACACACACACATGCACAC 71
Db 109 CACACACACACACACACATGCACAC 135

RESULT 6
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; Sequence 76927, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 76927
; LENGTH: 201
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-995-561-76927

Query Match 13.0%; Score 27; DB 6; Length 201;
Best Local Similarity 100.0%; Pred. No. 2.7e-05;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 45 CACACACACACACACACATGCACAC 71
Db 169 CACACACACACACACACATGCACAC 195

RESULT 7
US-10-995-561-77405
; Sequence 77405, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	50	24.2	1026	3	US-09-866-987-1
3	37	17.9	52138	10	US-11-166-990-75
4	36	17.4	67093	8	US-10-417-375-33
5	33	15.9	339234	7	US-10-322-696-73
6	32	15.5	447	8	US-10-674-124A-555
7	32	15.5	1742	4	US-09-925-065A-678678
8	32	15.5	39835	6	US-10-085-117-277
9	32	15.5	70019	7	US-10-322-281-823
10	32	15.5	77530	7	US-10-322-281-265
11	31	15.0	882	4	US-09-925-065A-72245
12	31	15.0	882	4	US-09-925-065A-72246
13	31	15.0	1475	4	US-09-925-065A-670284
14	31	15.0	1475	4	US-09-925-065A-670285
15	31	15.0	1475	4	US-09-925-065A-670286
16	30	14.5	402	3	US-09-983-965-5596
17	29	14.0	253	8	US-10-674-124A-6084
18	29	14.0	505	5	US-10-027-632-6710
19	29	14.0	505	6	US-10-027-632-6710
20	29	14.0	609	5	US-10-027-632-222642
21	29	14.0	609	6	US-10-027-632-222642
22	29	14.0	611	4	US-09-925-065A-588742
23	29	14.0	1194	5	US-10-027-632-119333

C 24	29	14.0	1194	5	US-10-027-632-119334	Sequence 119334,
C 25	29	14.0	1194	5	US-10-027-632-119335	Sequence 119335,
C 26	29	14.0	1194	5	US-10-027-632-119333	Sequence 119333,
C 27	29	14.0	1194	6	US-10-027-632-119334	Sequence 119334,
C 28	29	14.0	1194	6	US-10-027-632-119335	Sequence 119335,
C 29	29	14.0	1249	4	US-09-925-065A-667972	Sequence 667972,
C 30	29	14.0	1703	4	US-09-925-065A-76909	Sequence 76909, A
C 31	29	14.0	1724	4	US-09-925-065A-78157	Sequence 78157, A
C 32	29	14.0	1724	4	US-09-925-065A-78158	Sequence 78158, A
C 33	29	14.0	4361	10	US-11-097-143-5671	Sequence 5671, Ap
C 34	29	14.0	168050	9	US-10-939-321-1	Sequence 1, Appl
C 35	28	13.5	261	8	US-10-674-124A-16843	Sequence 16843, A
C 36	28	13.5	327	8	US-10-674-124A-13270	Sequence 13270, A
C 37	28	13.5	355	8	US-10-674-124A-4507	Sequence 4507, Ap
C 38	28	13.5	454	4	US-09-925-065A-464152	Sequence 464152,
C 39	28	13.5	464	4	US-09-925-065A-556697	Sequence 556697,
C 40	28	13.5	502	4	US-09-925-065A-835230	Sequence 835230,
C 41	28	13.5	517	4	US-09-925-065A-763473	Sequence 763473,
C 42	28	13.5	517	4	US-09-925-065A-763474	Sequence 763474,
C 43	28	13.5	760	4	US-09-925-065A-714119	Sequence 714119,
C 44	28	13.5	881	5	US-10-027-632-154764	Sequence 154764,
C 45	28	13.5	881	6	US-10-027-632-154764	Sequence 27553, A
C 46	28	13.5	22788	10	US-11-097-143-27553	Sequence 861, App
C 47	28	13.5	33916	7	US-10-322-281-861	Sequence 24, Appl
C 48	28	13.5	39699	7	US-10-322-281-24	Sequence 17854, A
C 49	28	13.5	49431	10	US-11-097-143-17854	Sequence 16, Appl
C 50	28	13.5	96593	3	US-09-997-722-16	

ALIGNMENTS

RESULT 1  
US-10-674-124A-2  
; Sequence 2, Application US/10674124A  
; Publication No. US20040197797A1  
; GENERAL INFORMATION:  
; APPLICANT: INOKO, Hidetoshi  
; APPLICANT: TAMIYA, Gen  
; TITLE OF INVENTION: GENE MAPPING METHOD USING MICROSATELLITE  
; FILE OF INVENTION: GENETIC POLYMORPHISM MARKERS  
; FILE REFERENCE: ORIN-003CIP  
; CURRENT APPLICATION NUMBER: US/10/674,124A  
; CURRENT FILING DATE: 2003-09-26  
; PRIOR APPLICATION NUMBER: 10/257,511  
; PRIOR FILING DATE: 2003-03-07  
; PRIOR APPLICATION NUMBER: PCT/JP00/07621  
; PRIOR FILING DATE: 2000-10-30  
; PRIOR APPLICATION NUMBER: JP2000-112699  
; PRIOR FILING DATE: 2000-04-13  
; PRIOR APPLICATION NUMBER: JP2002-327516  
; PRIOR FILING DATE: 2002-09-28  
; PRIOR APPLICATION NUMBER: JP2002-383869  
; PRIOR FILING DATE: 2002-12-09  
; NUMBER OF SEQ ID NOS: 27110  
; SEQ ID NO 2  
; LENGTH: 207  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; OTHER INFORMATION: Located on chromosome 1  
; FEATURE:  
; OTHER INFORMATION: Distance between a terminus base of telomere on  
; OTHER INFORMATION: chromosomal short arm and 5'-terminus of this base  
; OTHER INFORMATION: sequence : 100269  
; FEATURE:  
; OTHER INFORMATION: Distance between 3'-terminus of neighbour sequence of  
; OTHER INFORMATION: sequence listing upward to telomere on chromosomal short arm and  
; OTHER INFORMATION: 5'-terminus of this base sequence : 91592

US-10-674-124A-2

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Query Match      100.0%; Score 207; DB 8; Length 207;
Best Local Similarity 100.0%; Pred. No. 1e-100;
Matches 207; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AACCAAGTCTTAGCAGACGCGCTCCCTCAGGATCGAGGCACACGACACACACACACA 60
Db 1 AACCAAGTCTTAGCAGACGCGCTCCCTCAGGATCGAGGCACACGACACACACACACA 60

Qy 61 CACATGCACGCGACACACATGAACACACATGGAGCGCGGAACACACACATGCACAGTA 120
Db 61 CACATGCACGCGACACACATGAACACACATGGAGCGCGGAACACACACATGCACAGTA 120

Qy 121 CACACGTGTGCTGACACGCGGATGCTGGCCAGGGCTCACACCTCCAAACGGGGTCTTG 180
Db 121 CACACGTGTGCTGACACGCGGATGCTGGCCAGGGCTCACACCTCCAAACGGGGTCTTG 180

Qy 181 GCAGCCACGCGGTACACAGACTCAAT 207
Db 181 GCAGCCACGCGGTACACAGACTCAAT 207

RESULT 2
US-09-866-987-1/c
; Sequence 1, Application US/09866987
; Patent No. US20020090703A1
; GENERAL INFORMATION:
; APPLICANT: PLOWMAN, GREGORY D.
; APPLICANT: MARTINEZ, RICARDO
; APPLICANT: WHYTE, DAVID
; APPLICANT: MANNING, GERARD
; APPLICANT: SUDARSANAM, SUCHA
; APPLICANT: CAENPEEL, SEAN
; APPLICANT: HILL, RON
; APPLICANT: FLANAGAN, PETER
; TITLE OF INVENTION: MAMMALIAN PROTEIN PHOSPHATASES
; FILE REFERENCE: 038602/1180
; CURRENT APPLICATION NUMBER: US/09/866,987
; CURRENT FILING DATE: 2001-05-30
; PRIOR FILING DATE: 60/208,291
; PRIOR FILING DATE: 2000-05-30
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 1026
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: phosphatase nucleotide
US-09-866-987-1

Query Match      24.2%; Score 50; DB 3; Length 1026;
Best Local Similarity 100.0%; Pred. No. 1.1e-16;
Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 158 CACCACTCCAAACGGGGTCTTGGCAGCCCGGGTACCAAGCTCAAT 207
Db 323 CACCACTCCAAACGGGGTCTTGGCAGCCCGGGTACCAAGCTCAAT 274

RESULT 3
US-11-166-990-75
; Sequence 75, Application US/11166990
; Publication No. US20050239125A1
; GENERAL INFORMATION:
; APPLICANT: Hodges, Timothy A.
; TITLE OF INVENTION: METHODS FOR GENOTYPE SCREENING
; FILE REFERENCE: 023131.41500
; CURRENT APPLICATION NUMBER: US/11/166,990
; CURRENT FILING DATE: 2005-06-24
; PRIOR APPLICATION NUMBER: 60/230,371
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 09/945,952
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Query Match      17.9%; Score 37; DB 10; Length 52138;
Best Local Similarity 100.0%; Pred. No. 5.6e-10;
Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 16029 CACACACACACACACACATGCACATGCACACGACACACAT 16065

RESULT 4
US-10-417-375-33/c
; Sequence 33, Application US/10417375
; Publication No. US20040219528A1
; GENERAL INFORMATION:
; APPLICANT: David W. Morris
; APPLICANT: Marc Malandro
; TITLE OF INVENTION: Novel Therapeutic Targets in Cancer
; FILE REFERENCE: 529452001600
; CURRENT APPLICATION NUMBER: US/10/417,375
; CURRENT FILING DATE: 2003-04-15
; NUMBER OF SEQ ID NOS: 176
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 33
; LENGTH: 67093
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(67093)
; OTHER INFORMATION: n = A,T,C or G
US-10-417-375-33

Query Match      17.4%; Score 36; DB 8; Length 67093;
Best Local Similarity 100.0%; Pred. No. 1.9e-09;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 45 CACACACACACACACACATGCACATGCACACGACACACA 80
Db 29466 CACACACACACACACACATGCACATGCACACGACACACA 29431

RESULT 5
US-10-322-696-73/c
; Sequence 73, Application US/10322696
; Publication No. US20040166490A1
; GENERAL INFORMATION:
; APPLICANT: Morris, David W.
; APPLICANT: Malandro, Marc
; TITLE OF INVENTION: NOVEL THERAPEUTIC TARGETS IN CANCER
; FILE REFERENCE: 529452001200
; CURRENT APPLICATION NUMBER: US/10/322,696
; CURRENT FILING DATE: 2003-10-17
; NUMBER OF SEQ ID NOS: 186
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 73
; LENGTH: 339234
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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

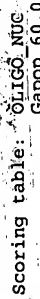
OM nucleic - nucleic search, using sw model

Run on: December 14, 2005, 03:22:04 ; Search time 67.3596 Seconds  
(without alignments)  
5462.552 Million cell updates/sec

Title: US-10-674-124A-2

Perfect score: 207

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Scoring table: 

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Word size: 6

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 50 summaries

Database : Issued Patents NA:\*

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- 5: /cgn2\_6/ptodata/1/ina/H COMB.seq:\*
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- 9: /cgn2\_6/ptodata/1/ina/BACKFILES.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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C 2	32	15.5	601	3	US-09-949-016-132718
C 3	32	15.5	601	3	US-09-949-016-132719
C 4	32	15.5	601	3	US-09-949-016-132720
C 5	32	15.5	194714	3	US-09-949-016-11869
C 6	32	15.5	196714	3	US-09-949-016-15474
C 7	30	14.5	601	3	US-09-949-016-109508
C 8	30	14.5	601	3	US-09-949-016-126979
C 9	30	14.5	601	3	US-09-949-016-126980
C 10	30	14.5	32202	3	US-09-949-016-15357
C 11	30	14.5	67581	3	US-09-949-016-14768
C 12	29	14.5	67843	3	US-09-949-016-14760
C 13	29	14.0	175236	3	US-09-949-016-14353
C 14	28	13.5	601	3	US-09-949-016-62776
C 15	28	13.5	601	3	US-09-949-016-62777
C 16	28	13.5	601	3	US-09-949-016-62778
C 17	28	13.5	601	3	US-09-949-016-62779
C 18	28	13.5	601	3	US-09-949-016-192212
C 19	28	13.5	601	3	US-09-949-016-192213
C 20	28	13.5	13948	3	US-09-949-016-13023
C 21	28	13.5	90766	3	US-09-949-016-17230
C 22	28	13.5	103792	3	US-09-949-016-13553
C 23	28	13.5	103993	3	US-09-949-016-12317
C 24	27	13.0	44	3	US-09-443-199C-1019

C 25	27	13.0	48	3	US-09-443-199C-1017	Sequence 1017, Ap
C 26	27	13.0	170	3	US-09-513-999C-23415	Sequence 23415, A
C 27	27	13.0	279	3	US-09-232-785-257	Sequence 257, App
C 28	27	13.0	286	3	US-09-513-999C-385	Sequence 385, App
C 29	27	13.0	310	3	US-09-328-111-715	Sequence 715, App
C 30	27	13.0	314	3	US-09-513-999C-14774	Sequence 14774, A
C 31	27	13.0	333	3	US-09-898-165B-29	Sequence 29, Appl
C 32	27	13.0	568	3	US-09-270-767-6074	Sequence 6074, Ap
C 33	27	13.0	568	3	US-09-270-767-21356	Sequence 21356, A
C 34	27	13.0	587	3	US-09-232-785-336	Sequence 336, App
C 35	27	13.0	601	3	US-09-949-016-58095	Sequence 58095, A
C 36	27	13.0	601	3	US-09-949-016-58096	Sequence 58096, A
C 37	27	13.0	601	3	US-09-949-016-141439	Sequence 141439, A
C 38	27	13.0	601	3	US-09-949-016-142850	Sequence 142850, A
C 39	27	13.0	601	3	US-09-949-016-142851	Sequence 142851, A
C 40	27	13.0	601	3	US-09-949-016-152327	Sequence 152327, A
C 41	27	13.0	601	3	US-09-949-016-162901	Sequence 162901, A
C 42	27	13.0	601	3	US-09-949-016-162902	Sequence 162902, A
C 43	27	13.0	601	3	US-09-949-016-192840	Sequence 192840, A
C 44	27	13.0	601	3	US-09-949-016-198491	Sequence 198491, A
C 45	27	13.0	601	3	US-09-949-016-198492	Sequence 198492, A
C 46	27	13.0	5578	2	US-08-081-610-2	Sequence 2, Appli
C 47	27	13.0	9950	3	US-09-949-016-12075	Sequence 12075, A
C 48	27	13.0	9950	3	US-09-949-016-14226	Sequence 14226, A
C 49	27	13.0	16442	3	US-08-781-891-208	Sequence 208, App
C 50	27	13.0	16442	3	US-09-618-166-208	Sequence 208, App

ALIGNMENTS

RESULT 1  
US-09-513-999C-8748/c  
; Sequence 8748, Application US/09513999C  
; Patent No. 6783961  
; GENERAL INFORMATION:  
; APPLICANT: Dumas Milne Edwards, J.B.  
; APPLICANT: Duclert, A.  
; APPLICANT: Giordano, J.Y.  
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.  
; Patent No. 6783961  
; FILE REFERENCE: 59. US2.REG  
; CURRENT APPLICATION NUMBER: US/09/513.999C  
; CURRENT FILING DATE: 2000-02-24  
; PRIOR APPLICATION NUMBER: US 60/122,487  
; PRIOR FILING DATE: 1999-02-26  
; NUMBER OF SEQ ID NOS: 36681  
; SOFTWARE: Patent.pm  
; SEQ ID NO 8748  
; LENGTH: 268  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: 168  
; OTHER INFORMATION: k=g or t  
US-09-513-999C-8748

Query Match 15.9%; Score 33; DB 3; Length 268;  
Best Local Similarity 100.0%; Pred. No. 1.5e-06;  
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 50 ACACACACACACATGCACACGACACACATG 82  
Db 71 ACACACACACACATGCACACGACACACATG 39

RESULT 2  
US-09-949-016-132718  
; Sequence 132718, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.

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; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 132718
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-132718

Query Match      15.5%; Score 32; DB 3; Length 601;
Best Local Similarity 100.0%; Pred. No. 4.3e-06;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      45 CACACACACACACACATGCACACGCACA 76
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RESULT 3
US-09-949-016-132719
; Sequence 132719, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 132719
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-132719

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Best Local Similarity 100.0%; Pred. No. 4.3e-06;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 4
US-09-949-016-132720
; Sequence 132720, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
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; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 132720
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-132720

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Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 5
US-09-949-016-11869/c
; Sequence 11869, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11869
; LENGTH: 194714
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-11869

Query Match      15.5%; Score 32; DB 3; Length 194714;
Best Local Similarity 100.0%; Pred. No. 2.5e-06;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      45 CACACACACACACACATGCACACGCACA 76
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RESULT 6
US-09-949-016-15474/c
; Sequence 15474, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 14, 2005, 04:20:34 ; Search time 1927.59 Seconds  
(without alignments)  
5024.367 Million cell updates/sec

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Post-processing: Listing first 50 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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5	36	17.4	840	11	CR169879
6	36	17.4	1042	11	CNS04CZG
7	36	17.4	1049	11	CNS05DIS
8	35	16.9	283	10	BX972640
9	35	16.9	494	9	AZ407953
10	35	16.9	496	9	AZ024543
11	35	16.9	611	9	AZ380969
12	35	16.9	1201	10	AG338469
13	34	16.4	376	3	BI534913
14	34	16.4	415	6	CB799941
15	34	16.4	486	10	BX177437
16	34	16.4	502	9	BT148403
17	34	16.4	510	11	FR0043263
18	34	16.4	537	9	AZ006109
19	34	16.4	572	11	FR0043899
20	34	16.4	600	11	FR0041672
21	34	16.4	618	11	FR0043913
22	34	16.4	713	9	BZ282696

C 23	34	16.4	754	11	CR128435
C 24	34	16.4	769	9	BZ139452
C 25	34	16.4	792	9	BZ282602
C 26	34	16.4	804	11	CR190843
C 27	34	16.4	901	7	CK401939
C 28	33	15.9	307	9	AZ022678
C 29	33	15.9	475	9	AQ285135
C 30	33	15.9	523	9	AQ148705
C 31	33	15.9	622	9	AZ004814
C 32	33	15.9	629	9	AQ194800
C 33	33	15.9	700	10	AG341713
C 34	33	15.9	739	10	AG516767
C 35	33	15.9	888	6	CA511475
C 36	33	15.9	1101	10	CNS014NB
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C 43	32	15.5	424	9	BZ251046
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ALIGNMENTS

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1M0395C05F Mouse 10kb plasmid UUGCLM library Mus musculus genomic  
clone UUGC1M0395C05 F, genomic survey sequence.  
AZ587362 GI:11709552  
GSS.  
Mus musculus (house mouse)  
Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;  
Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 671)  
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,  
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,  
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von  
Niederhausern, A. and Wright, D., Weiss, R.  
Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts  
Unpublished (2000)  
Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: dunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0395 row: C column: 05  
Seq primer: CGTTGTAAACGACGCCAGT  
Class: plasmid ends  
High quality sequence stop: 671.  
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/strain="C57BL/6J"  
/db\_xref="taxon:10090"

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

source

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/clone="UUGC1M0395C05"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 [gi|4732114|gb|AF129072.1], a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN
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Db 282 CACACACACACACACATGCACGACACACATG 319

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DEFINITION RPCI-24-118H15-TV RPCI-24 Mus musculus genomic clone
A2733430
ACCESSION A2733430
VERSION A2733430.1 GI:12497660
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 287)
Zhao,S., Nieman,W., Malek,J., Shatsman,S., Akinret,B., Levins,M.,
Teegaye,G., Geer,K., Krol,M., Shvartsbeyn,A., Gebregeorgis,E.,
Russell,D., de Jong,P. and Fraser,C.M.
Mouse BAC End Sequences from Library RPCI-24
Unpublished (1999)
Other GSSs: RPCI-24-118H15.TJ
Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
Email: szhao@tigr.org
Clones are derived from the mouse BAC library RPCI-24. For BAC
library availability, please contact Pieter de Jong
(pdejong@mail.cho.org). Clones may be purchased from BACPAC
Resources (http://www.choi.org/bacpac/orderingframe.htm). BAC end
page: http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html
Plate: 118 row: H column: 15
Seq primer: T7
Class: BAC ends.
Location/Qualifiers
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/sex="Male"
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/clone_lib="RPCI-24"
/notes="Vector: PTARBAC1; Site 1: BamH1; Site 2: BamH1;
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library was cloned in the pTARBAC1 cloning vector at the
BamH1 sites using MboI partially digested male C57BL/6J
DNA."

ORIGIN
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Best Local Similarity 100.0%; Pred. No. 3.5e-07;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DEFINITION UI-R-CNI-cma-e-19-0-UI.s1 UI-R-CNI Rattus norvegicus cDNA clone
BQ194283
ACCESSION BQ194283
VERSION BQ194283.1 GI:20369834
KEYWORDS EST.
SOURCE Rattus norvegicus (Norway rat)
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Rattus.
1 (bases 1 to 478)
Bonaldo,M.F., Lennon,G. and Soares,M.B.
Normalization and subtraction: two approaches to facilitate gene
discovery
Genome Res. 6 (9), 791-806 (1996)
8889548
Contact: Soares, MB
Coordinated Laboratory for Computational Genomics
University of Iowa
375 Newton Road, 4156 MEBRF, Iowa City, IA 52242, USA
Tel: 319 335 8250
Fax: 319 335 9565
Email: bento-soares@uiowa.edu
The sequence contained an oligo-dT track that was present in the
oligonucleotide that was used to prime the synthesis of first
strand cDNA and therefore this may represent a bonafide poly A
tail. The sequence tag present in the cDNA between the NotI site
and the oligo-dT track served to identify it as a clone from the
normalized fundus library cDNA Library Preparation: M.B. Soares Lab
Clone distribution: clones will be available through Research
Genetics (www.resgen.com) The following repetitive elements were
found in this cDNA sequence: 14-84, >(CA)n#Simple_repeat 86-356,
>B4A#SINE/B4
Seq primer: M13 Forward
POLYA=Yes.
Location/Qualifiers
1. .478
/organism="Rattus norvegicus"
/mol_type="mRNA"
/strain="Sprague-Dawley"
/db_xref="taxon:10116"
/clone="UI-R-CNI-cma-e-19-0-UI"
/dev_stage="adult"
/lab_host="DHI0B (Life Technologies)"
/clone_lib="UI-R-CNI"
/notes="Vector: pT7T3D-Pac (Pharmacia) with a modified
polylinker; Site 1: Not I; Site 2: Eco RI; The UI-R-CNI
library is a subtracted library derived from the following

```

Result No.	Query			ID	Description
	Score	Match	Length		
C 1	50	24.2	1026	6	ABA94424 Human pro
C 2	36	17.4	67093	13	ABD32671 Mouse can
C 3	33	15.9	268	3	AAC04673 Human sec
C 4	33	15.9	90220	6	ABK83576 Human CDN
C 5	33	15.9	392234	12	ADQ59437 Human can
C 6	33	15.9	339234	14	ADZ13744 Murine ca
C 7	32	15.5	3267	12	ADK52131 Mouse ato
C 8	32	15.5	70019	13	ABD33601 Murine ca
C 9	32	15.5	77530	13	ABD33240 Murine ca
C 10	31	15.0	972	10	ADC12701 Human GPC
C 11	31	15.0	77287	9	AAD58261 Murine tu
C 12	31	15.0	167739	9	AAD58258 Murine tu
C 13	30	14.5	402	8	ABX55667 Bovine ES
C 14	30	14.5	38920	12	ADQ97252 Mouse can
C 15	29	14.0	407	4	AAI90660 Human pol
C 16	29	14.0	4361	4	ABL05620 Drosophil
C 17	29	14.0	110000	12	ADQ97047 Mouse can
C 18	29	14.0	151052	12	ADQ97526 Mouse can
C 19	28	13.5	694	4	AAI188049 Human pol

```
XX WPI; 2002-114340/15.
DR P-FSDB; ABB07302.
XX
XX New phosphatase polypeptides for treating e.g., cancers, immune-related
PT diseases and disorders, cardiovascular diseases, or brain or neuronal-
PT associated diseases.
XX
XX Claim 28; Fig 1A; 161pp; English.
XX
XX The invention relates to human protein phosphatase polypeptides and
CC polynucleotides. The phosphatase polypeptides are useful for diagnosing
CC and treating various phosphatase-related diseases and conditions, such as
CC cancers, immune-related diseases and disorders, cardiovascular diseases
CC (e.g., reperfusion restenosis), brain or neuronal-associated diseases,
CC metabolic disorders (e.g., diabetes or obesity), central or peripheral
CC nervous system diseases and conditions (e.g., pain, migraine, mood
CC disorders, hypotension, or hypertension), psychotic and neurological
CC disorders (e.g., anxiety, schizophrenia), neurodegenerative diseases
CC (e.g., Alzheimer's or Parkinson's disease), infections caused by viral
CC (e.g., human immunodeficiency virus (HIV)), bacterial, fungal or prion-
CC agents, ocular diseases, macular degeneration, and inflammatory disorders
CC (e.g., rheumatoid arthritis, multiple sclerosis, osteoarthritis). The
CC polypeptides may also be used for screening for small molecule compounds
CC that inhibit the catalytic activity of the encoded protein phosphatase
CC with potential use for treating the above-mentioned diseases, for
CC generating antibodies or hybridomas, and as a diagnostic tool for
CC detecting a disease or disorder. Genetic sequences of phosphatases are
CC useful in gene therapy. The present sequence represents a cDNA encoding a
CC novel human protein tyrosine phosphatase (PTP)-like phosphatase
CC polypeptide SGP057
XX
XX Sequence 1026 BP; 176 A; 294 C; 393 G; 163 T; 0 U; 0 Other;
SQ
Query Match 24.2%; Score 50; DB 6; Length 1026;
Best Local Similarity 100.0%; Pred. No. 9.3e-15;
Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 158 CACCACTCCACGGGGGTCTGGCAGCCCGGGTACCGAGTCAAT 207
DB 323 CACCACTCCACGGGGGTCTGGCAGCCCGGGTACCGAGTCAAT 274
RESULT 2
ABD32671/c
ID ABD32671 standard; DNA; 67093 BP.
XX
XX ABD32671;
XX
XX 18-NOV-2004 (first entry)
XX
XX Mouse cancer-associated genomic DNA MD13-075.
XX
XX Mouse; ds; cancer-associated protein; gene; cytostatic; cancer;
XX leukaemia; lymphoma; CAP.
XX
XX Mus musculus.
XX
XX WO2004074320-A2.
XX
XX 02-SEP-2004.
XX
XX 17-FEB-2004; 2004WO-US004730.
XX
XX 14-FEB-2003; 2003US-00367094.
XX 14-MAR-2003; 2003US-00388838.
XX 15-APR-2003; 2003US-00417375.
XX 13-JUN-2003; 2003US-00461862.
XX 15-SEP-2003; 2003US-00663431.
XX 15-DEC-2003; 2003US-00737318.
XX (SAGR-) SAGRES DISCOVERY INC.
XX
XX Morris DW, Morris DW, Malandro MS;
XX WPI; 2004-652914/63.
XX
XX New isolated cancer-associated polynucleotides and polypeptides useful
PT for diagnosing, preventing or treating cancers, especially lymphoma and
PT leukemia, or in screening for agents that modulate cancer.
XX
XX disclosure; seqid 218; 310pp; English.
XX
XX The invention relates to an isolated nucleic acid comprising at least 10
CC contiguous nucleotides of any of the 233 polynucleotide sequences given
CC in the specification, or its complement. The nucleic acids encode cancer-
CC associated proteins. Also included are an expression vector comprising
CC the isolated nucleic acid cited above, a host cell comprising the above
CC recombinant nucleic acid or expression vector, a microarray for detecting
CC a cancer-associated (CA) nucleic acid comprising at least one probe
CC comprising at least 10 contiguous nucleotides of any of the above-
CC mentioned nucleotide sequences, an isolated polypeptide (encoded within
CC an open reading frame of a CA sequence selected from any of the 95
CC polynucleotide sequences as mentioned in the specification, or its
CC complement), an isolated antibody, (or its antigen binding fragment) that
CC binds to the above polypeptide, a hybridoma that produces the above
CC monoclonal antibody, a pharmaceutical composition comprising the above
CC antibody and a pharmaceutical excipient, a kit for detecting cancer
CC cells (comprising the antibody cited above, methods for diagnosing cancer
CC or for detecting the presence or absence of cancer cells in an
CC individual, a method for inhibiting growth of cancer cells in an
CC individual, a method for delivering a therapeutic agent to cancer cells
CC in an individual, an electronic library comprising the above
CC polynucleotide or polypeptide (or their fragments), methods of screening
CC for anticancer activity or for a bioactive agent capable of modulating
CC the activity of a CA protein (CAP), methods for detecting cancer
CC associated with expression of a polypeptide in a test cell sample, a
CC method for treating cancers and a method for inhibiting the expression of
CC CA gene in a cell. The composition and methods are useful for detecting,
CC diagnosing, preventing and treating cancers, especially lymphoma and
CC leukaemia. These may also be used in screening for agents that modulate
CC cancer. The present sequence is a mouse CAP genomic sequence. Note: The
CC sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 67093 BP; 17235 A; 15136 C; 16131 G; 18531 T; 0 U; 60 Other;
SQ
Query Match 17.4%; Score 36; DB 13; Length 67093;
Best Local Similarity 100.0%; Pred. No. 6.4e-08;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 45 CACACACACACACACACATGCACACGACACACA 80
DB 29466 CACACACACACACACACATGCACACGACACACA 29431
RESULT 3
AAC04673/c
ID AAC04673 standard; cDNA; 268 BP.
XX
XX AAC04673;
XX
XX 06-OCT-2000 (first entry)
XX
XX Human secreted protein 5' EST, SEQ ID NO: 8748.
XX
XX Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;
XX gene therapy; chromosome mapping; ss.
XX
XX Homo sapiens.
XX
XX EF1033401-A2.
XX
XX 06-SEP-2000.
XX
```

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: December 13, 2005, 22:13:37 ; Search time 1202.94 Seconds  
(without alignments)  
9781.550 Million cell updates/sec

Title: US-10-674-124A-2  
Perfect score: 207  
Sequence: 1 aaccagtgcttagcagcgc.....agcgggtaccagagctcaat 207

Scoring table: OLIGO NUC  
Gapop 60.0 , Gapext 60.0

Searched: 5883141 seqs, 28421725653 residues

Word size : 0  
Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Listing first 50 summaries

Database : GenEmbl.\*  
1: gb\_bai.\*  
2: gb\_in.\*  
3: gb\_env.\*  
4: gb\_om.\*  
5: gb\_ov.\*  
6: gb\_pat.\*  
7: gb\_ph.\*  
8: gb\_pr.\*  
9: gb\_ro.\*  
10: gb\_sts.\*  
11: gb\_sv.\*  
12: gb\_un.\*  
13: gb\_vl.\*  
14: gb\_htg.\*  
15: gb\_pl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	207	100.0	207	AB151030	AB151030 Homo sapi
C 2	207	100.0	130979	AL330719	AL330719 Human DNA
C 3	161	77.8	327883	14 BX571684	BX571684 Homo sapi
C 4	50	24.2	1026	6 AX352512	AX352512 Sequence
C 5	44	21.3	224653	14 AC149246	AC149246 Otolomur
C 6	43	20.8	159031	9 CR339053	CR339053 Danio rer
C 7	39	18.8	199235	9 AC110164	AC110164 Mus muscu
C 8	38	18.4	96128	9 AL663077	AL663077 Mus muscu
C 9	38	18.4	142364	9 AC156951	AC156951 Mus muscu
C 10	38	18.4	149347	14 AC131813	AC131813 Rattus no
C 11	38	18.4	168635	14 AC142061	AC142061 Rattus no
C 12	38	18.4	174894	14 AC118979	AC118979 Rattus no
C 13	38	18.4	212022	14 AC134726	AC134726 Rattus no
C 14	38	18.4	217297	14 AC114141	AC114141 Rattus no
C 15	38	18.4	225524	9 AC133489	AC133489 Mus muscu
C 16	38	18.4	226183	14 AC123101	AC123101 Rattus no
C 17	38	18.4	244692	14 AC128181	AC128181 Rattus no
C 18	38	18.4	244707	14 AC098994	AC098994 Rattus no

19	17.9	150109	9	AC132334	AC132334 Mus muscu
20	17.9	175275	14	AC091883	AC091883 Homo sapi
21	17.9	178488	9	AC123548	AC123548 Mus muscu
22	17.9	181955	8	AC010546	AC010546 Homo sapi
23	17.9	203193	14	AC128175	AC128175 Rattus no
24	17.9	271477	14	AC121616	AC121616 Rattus no
25	17.4	258	10	AU048719	AU048719 Rattus no
26	17.4	446	10	G46315	G46315 Z8506_1 Zeb
27	17.4	67093	6	CQ869797	CQ869797 Sequence
28	17.4	107113	14	AC142559	AC142559 Takifugu
29	17.4	110000	14	AC110125	AC110125 1
30	17.4	110000	14	AC128511	AC128511 2
31	17.4	110000	14	AC130034	AC130034 1
32	17.4	115003	5	EX005089	EX005089 Zebrafish
33	17.4	120487	9	AC103637	AC103637 Mus muscu
34	17.4	131042	9	AC110166	AC110166 Mus muscu
35	17.4	135686	14	AC140742	AC140742 Rattus no
36	17.4	135800	14	AF523316	AF523316 Canis fam
37	17.4	143147	14	AC141204	AC141204 Rattus no
38	17.4	146823	14	AC161294	AC161294 Otolomur
39	17.4	147370	9	AC123039	AC123039 Mus muscu
40	17.4	148976	14	AC130201	AC130201 Mus muscu
41	17.4	153492	9	AC124391	AC124391 Mus muscu
42	17.4	154614	14	CR855263	CR855263 Danio rer
43	17.4	155547	9	AC132595	AC132595 Mus muscu
44	17.4	157393	9	AC124199	AC124199 Mus muscu
45	17.4	160832	14	AC142051	AC142051 Rattus no
46	17.4	162572	14	AC166627	AC166627 Sorex ara
47	17.4	164485	9	AC122513	AC122513 Mus muscu
48	17.4	165196	9	AL596123	AL596123 Mouse DNA
49	17.4	166292	9	AC123049	AC123049 Mus muscu
50	17.4	169501	9	AC125100	AC125100 Mus muscu

ALIGNMENTS

RESULT 1

AB151030/c

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

AB151030 Homo sapiens DNA, STS on chromosome 1, D1S14251, sequence tagged site.  
207 bp DNA linear STS 02-APR-2005

AB151030 GI:62171848

AB151030.1

STS.

Homo sapiens (human)

Homo sapiens

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

Hominidae; Homo.

1

Tamiya, G., Shinya, M., Ikuta, T., Makino, S., Matsumoto, T., Mano, S.,

Furugaki, K., Ando, S., Nozaki, Y., Yukawa, W., Nakashige, R.,

Yamaguchi, D., Ishibashi, H., Yonekura, M., Nakami, Y., Takayama, S.,

Endo, T., Saruwatari, T., Yagura, M., Yoshikawa, Y., Fujimoto, K.,

Oka, A., Chiku, S., Linsen, S. E., Giphart, M. J., Bahram, S.,

Kulski, Y. J., Fukazawa, T., Hashimoto, H., Hoshina, Y., Suzuki, Y.,

Hotta, T., Mochida, J., Minezaki, T., Komai, K., Shiozawa, S.,

Taniguchi, A., Yamanaka, H., Kamatani, N., Imanishi, T., Gojobori, T.

and Inoko, H.

A Whole Genome Association Study of Rheumatoid Arthritis using

27,039 Microsatellite Markers

Unpublished

2 (bases 1 to 207)

Tamiya, G., Makino, S., Fujimoto, K., Oka, A., Hayashi, H., Denda, A.,

Linssen, S. E., Ikuta, T., Shinya, M., Endo, T., Tomizawa, M., Tokubo, E.,

Sato, R., Takaki, A., Nagatsuka, Y., Watanabe, H., Adachi, S.,

Makino, Y., Nakano, S., Yamamoto, A., Yoshida, K., Okamoto, K.,

Yamaguchi, D., Ishibashi, H., Yonekura, M., Takayama, S., Nakami, Y.,

Saruwatari, T., Brand, A., van Hilten, J. A., van de Watering, L. M.,

Giphart, M. J., Bahram, S., Kulski, Y. J. and Inoko, H.

Direct Submission

Submitted (12-DEC-2003) Hidetoshi Inoko, Tokai University School of

Medicine, Department of Genetic Information; Bohseidai, Isehara, Kanagawa, 259-1193, Japan (E-mail: hinokoe@is.icc.u-tokai.ac.jp, Tel: 81-463-93-1121, Fax: 81-463-94-8884)

**COMMENT**

Polymorphisms were confirmed by comparing with the pooled DNA typing data of 88 Dutch population or 100 Australian. When there was no significant difference between the Japanese and these Caucasians, individual typing was performed to confirm polymorphisms.

**FEATURES**

source

1. .207

/organism="Homo sapiens"

/mol\_type="genomic DNA"

/db\_xref="taxon:9606"

/chromosome="1"

/map="lp36.33"

/note="pooled DNA of 100 Japanese unrelated individuals sequence tagged site D1S14251"

1. 18

/note="5' primer: ATGTAGCTCTGTGATCCG"

/PCR\_conditions="denaturation 96degC 5 min, 57degC 1 min, 72degC 1 min; 40 cycles 96degC 45 sec, 57degC 45 sec, 72degC 1 min"

144. .163

/note="sequence tagged site D1S14251"

/rpt\_type=tandem

/rpt\_unit="tg"

complement(189. .207)

/note="3' primer: AACCACTGCTTAGCAGACG"

**primer\_bind**

1. 18

/note="5' primer: ATGTAGCTCTGTGATCCG"

/PCR\_conditions="denaturation 96degC 5 min, 57degC 1 min, 72degC 1 min; 40 cycles 96degC 45 sec, 57degC 45 sec, 72degC 1 min"

144. .163

/note="sequence tagged site D1S14251"

/rpt\_type=tandem

/rpt\_unit="tg"

complement(189. .207)

/note="3' primer: AACCACTGCTTAGCAGACG"

## ORIGIN

Query Match 100.0%; Score 207; DB 10; Length 207;

Best Local Similarity 100.0%; Pred. No. 1.7e-99;

Matches 207; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AACCACTGCTTAGCAGACGCGTCCCTCAGATGCGGCACACGACACACACACACA 60

Db 207 AACCACTGCTTAGCAGACGCGTCCCTCAGATGCGGCACACGACACACACACA 148

Qy 61 CACATGACACGCGCACACATGACACATGACGCGAACACACACATGACACGTA 120

Db 147 CACATGACACGCGCACACATGACACATGACGCGAACACACACATGACACGTA 88

Qy 121 CACAGTGTGTGACACGCGATGCTGGCGAGGCTCACACTCCAAACGGGGTCTG 180

Db 87 CACAGTGTGTGACACGCGATGCTGGCGAGGCTCACACTCCAAACGGGGTCTG 28

Qy 181 GCAGCCACGCGGTACACAGCTCAAT 207

Db 27 GCAGCCACGCGGTACACAGCTCAAT 1

**RESULT 2**

AL390719/c

**LOCUS**

AL390719 130979 bp DNA linear PRI 18-MAY-2005

**DEFINITION**

Human DNA sequence from clone Rp11-465B22 on chromosome 1 Contains a novel gene, a novel gene, a protein tyrosine phosphatase family pseudogene, a novel gene (FLJ20584), a novel gene, a novel gene, a novel gene (FLJ36119) and five CpG islands, complete sequence.

**ACCESSION**

AL390719

**VERSION**

AL390719.47 GI:31071457

**KEYWORDS**

HTG; FLJ20584; FLJ36119.

**SOURCE**

Homo sapiens (human)

**ORGANISM**

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homidae; Homo.

**REFERENCE**

1 (bases 1 to 130979)

**AUTHORS**

Matthews, L.

**TITLE**

Direct Submission

**JOURNAL**

Submitted (13-MAY-2005) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: vegas@sanger.ac.uk

**COMMENT**

Clone requests: clonerequest@sanger.ac.uk

On May 23, 2003 this sequence version replaced gi:30722520.

The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:

Em: EMBL; Sw: SWISSPROT; Tr: TREMBL; Wp: WORMPEP; Information on the WORMPEP database can be found at

http://www.sanger.ac.uk/Projects/C\_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 1, constructed by the Sanger Centre Chromosome 1 Mapping Group. Further information can be found at

http://www.sanger.ac.uk/HGP/Chr1

RP11-465B22 is from the library RP11-11.2 constructed by the group of Pieter de Jong. For further details see

http://www.choxi.org/bacpac/home.htm

VECTOR: pBACE3.6

----- Genome Center

Center: Wellcome Trust Sanger Institute

Center code: SC

Web site: http://www.sanger.ac.uk

Contact: vegas@sanger.ac.uk

-----

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one subclone; and the assembly was confirmed by restriction digest, except on the rare occasion of the clone being a YAC.

## FEATURES

## source

1. .130979

/organism="Homo sapiens"

/mol\_type="genomic DNA"

/db\_xref="taxon:9606"

/chromosome="1"

/clone="RP11-465B22"

/clone\_lib="RP11-11.2"

## misc\_feature

2000

/note="Clone right end: RP11-5407"

join(AL645608.30:186058..186658,2152..2379)

## gene

/locus\_tag="RP11-465B22.2-001"

join(AL645608.30:186058..186658,2152..2379)

## mRNA

/locus\_tag="RP11-465B22.2-001"

/product="putative novel transcript"

## gene

/note="match: ESTs: Em:BQ918995.1"

join(2167..2290,2571..2857,3301..3492,3581..3680,4443..4566,5678..5758,6657..6737,6960..7094,7668..7815,8299..8446)

## CDS

/locus\_tag="RP11-465B22.3-001"

/pseudo

join(2167..2290,2571..2857,3301..3492,3581..3680,4443..4566,5678..5758,6657..6737,6960..7094,7668..7815,8299..8446)

## gene

/note="match: proteins: Q9QVA8 Sw:P29350 Sw:P35235 Sw:P41499 Sw:Q06124 Tr:AAP36054 Tr:BAC81774 Tr:BAC81775 Tr:P81718 Tr:Q64509 Tr:Q72W17 Tr:Q92124 Tr:Q96HD7 Tr:Q9CT18 Tr:Q9UK67"

## gene

/product="protein tyrosine phosphatase family pseudogene"

join(2170..2292,4921..5547)

## gene

/locus\_tag="RP11-465B22.1-001"

join(AL645608.30:183584..183696,

## mRNA

AL645608.30:184130..184243,2170..2292,4921..5547)

/locus\_tag="RP11-465B22.1-005"

## mRNA

join(2170..2292,4921..5547)

/locus\_tag="RP11-465B22.1-001"

## mRNA

/product="novel transcript"

/note="match: ESTs: Em:BF035622.1 Em:BI601978.1 match: CDNAs: Em:BC033949.2"

## mRNA

join(AL645608.30:183584..183696,

## mRNA

AL645608.30:184130..184243,2170..2292,4921..5547)

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## mRNA

/product="novel transcript"

/note="match: ESTs: Em:BI601978.1"